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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: LeukoSite, Inc.
(B) STREET: 215 First Street
(C) CITY: Cambridge
(D) STATE/PROVINCE: Massachusetts
(E) COUNTRY: U.S.A.
(F) POSTAL CODE/ZIP: 02142
(G) TELEPHONE: (617) 621-9350
(I) TELEFAX: (617) 621-9349

(i) APPLICANT/INVENTOR:

(A) NAME: Michael J. Briskin
(B) STREET: 28 Harbell Street
(C) CITY: Lexington
(D) STATE/PROVINCE: Massachusetts
(E) COUNTRY: U.S.A.
(F) POSTAL CODE/ZIP: 02173

(i) APPLICANT/INVENTOR:

(A) NAME: Douglas J. Ringler
(B) STREET: 382 Ocean Avenue, #1008
(C) CITY: Revere
(D) STATE/PROVINCE: Massachusetts
(E) COUNTRY: U.S.A.
(F) POSTAL CODE/ZIP: 02151

(i) APPLICANT/INVENTOR:

(A) NAME: Dominic Picarella
(B) STREET: 2 North Bennet Court, #4
(C) CITY: Boston
(D) STATE/PROVINCE: Massachusetts
(E) COUNTRY: U.S.A.
(F) POSTAL CODE/ZIP: 02113

(i) APPLICANT/INVENTOR:

(A) NAME: Walter Newman
(B) STREET: 3 Durham Street, #3
(C) CITY: Boston
(D) STATE/PROVINCE: Massachusetts
(E) COUNTRY: U.S.A.
(F) POSTAL CODE/ZIP: 02115

(ii) TITLE OF INVENTION: Mucosal Vascular Addressins and Uses
Thereof

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
(B) STREET: Two Militia Drive
(C) CITY: Lexington
(D) STATE: Massachusetts
(E) COUNTRY: U.S.A.
(F) ZIP: 02173-4799

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(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/523,004
- (B) FILING DATE: 01-SEP-1995

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/386,857
- (B) FILING DATE: 10-FEB-1995

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Brook, David E.
- (B) REGISTRATION NUMBER: 22,592
- (C) REFERENCE/DOCKET NUMBER: LKS94-04A2 PCT

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 617-861-6240
- (B) TELEFAX: 617-861-9540

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1624 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GAT TTC GGA CTG GCC CTC CTG CTG GCG GGG CTT CTG GGG CTC CTC	48
Met Asp Phe Gly Leu Ala Leu Leu Leu Ala Gly Leu Leu Gly Leu Leu	
1 5 10 15	
CTC GGC CAG TCC CTC CAG GTG AAG CCC CTG CAG GTG GAG CCC CCG GAG	96
Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu Pro Pro Glu	
20 25 30	
CCG GTG GTG GCC GTG GCC TTG GGC GCC TCG CGC CAG CTC ACC TGC CGC	144
Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg	
35 40 45	

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CTG GCC TGC GCG GAC CGC GGG GCC TCG GTG CAG TGG CGG GGC CTG GAC Leu Ala Cys Ala Asp Arg Gly Ala Ser Val Gln Trp Arg Gly Leu Asp 50 55 60	192
ACC AGC CTG GGC GCG GTG CAG TCG GAC ACG GGC CGC AGC GTC CTC ACC Thr Ser Leu Gly Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr 65 70 75 80	240
GTG CGC AAC GCC TCG CTG TCG GCG GCC GGG ACC CGC GTG TGC GTG GGC Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val Cys Val Gly 85 90 95	288
TCC TGC GGG GGC CGC ACC TTC CAG CAC ACC GTG CAG CTC CTT GTG TAC Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Gln Leu Leu Val Tyr 100 105 110	336
GCC TTC CCG GAC CAG CTG ACC GTC TCC CCA GCA GCC CTG GTG CCT GGT Ala Phe Pro Asp Gln Leu Thr Val Ser Pro Ala Ala Leu Val Pro Gly 115 120 125	384
GAC CCG GAG GTG GCC TGT ACG GCC CAC AAA GTC ACG CCC GTG GAC CCC Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro Val Asp Pro 130 135 140	432
AAC GCG CTC TCC TTC TCC CTG CTC GTC GGG GGC CAG GAA CTG GAG GGG Asn Ala Leu Ser Phe Ser Leu Leu Val Gly Gly Gln Glu Leu Glu Gly 145 150 155 160	480
GCG CAA GCC CTG GGC CCG GAG GTG CAG GAG GAG GAG GAG GAG CCC CAG Ala Gln Ala Leu Gly Pro Glu Val Gln Glu Glu Glu Glu Glu Pro Gln 165 170 175	528
GGG GAC GAG GAC GTG CTG TTC AGG GTG ACA GAG CGC TGG CGG CTG CCG Gly Asp Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp Arg Leu Pro 180 185 190	576
CCC CTG GGG ACC CCT GTC CCG CCC GCC CTC TAC TGC CAG GCC ACG ATG Pro Leu Gly Thr Pro Val Pro Pro Ala Leu Tyr Cys Gln Ala Thr Met 195 200 205	624
AGG CTG CCT GGC TTG GAG CTC AGC CAC CGC CAG GCC ATC CCC GTC CTG Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala Ile Pro Val Leu 210 215 220	672
CAC AGC CCG ACC TCC CCG GAG CCT CCC GAC ACC ACC TCC CCG GAG CCT His Ser Pro Thr Ser Pro Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro 225 230 235 240	720
CCC AAC ACC ACC TCC CCG GAG TCT CCC GAC ACC ACC TCC CCG GAG TCT Pro Asn Thr Thr Ser Pro Glu Ser Pro Asp Thr Thr Ser Pro Glu Ser 245 250 255	768
CCC GAC ACC ACC TCC CAG GAG CCT CCC GAC ACC ACC TCC CAG GAG CCT Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Gln Glu Pro 260 265 270	816
CCC GAC ACC ACC TCC CAG GAG CCT CCC GAC ACC ACC TCC CCG GAG CCT Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro 275 280 285	864

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CCC GAC AAG ACC TCC CCG GAG CCC GCC CCC CAG CAG GGC TCC ACA CAC Pro Asp Lys Thr Ser Pro Glu Pro Ala Pro Gln Gln Gly Ser Thr His 290 295 300	912
ACC CCC AGG AGC CCA GGC TCC ACC AGG ACT CGC CGC CCT GAG ATC TCC Thr Pro Arg Ser Pro Gly Ser Thr Arg Thr Arg Arg Pro Glu Ile Ser 305 310 315 320	960
CAG GCT GGG CCC ACG CAG GGA GAA GTG ATC CCA ACA GGC TCG TCC AAA Gln Ala Gly Pro Thr Gln Gly Glu Val Ile Pro Thr Gly Ser Ser Lys 325 330 335	1008
CCT GCG GGT GAC CAG CTG CCC GCG GCT CTG TGG ACC AGC AGT GCG GTG Pro Ala Gly Asp Gln Leu Pro Ala Ala Leu Trp Thr Ser Ser Ala Val 340 345 350	1056
CTG GGA CTG CTG CTC CTG GCC TTG CCC ACG TAT CAC CTC TGG AAA CGC Leu Gly Leu Leu Leu Ala Leu Pro Thr Tyr His Leu Trp Lys Arg 355 360 365	1104
TGC CGG CAC CTG GCT GAG GAC GAC ACC CAC CCA CCA GCT TCT CTG AGG Cys Arg His Leu Ala Glu Asp Thr His Pro Pro Ala Ser Leu Arg 370 375 380	1152
CTT CTG CCC CAG GTG TCG GCC TGG GCT GGG TTA AGG GGG ACC GGC CAG Leu Leu Pro Gln Val Ser Ala Trp Ala Gly Leu Arg Gly Thr Gly Gln 385 390 395 400	1200
GTC GGG ATC AGC CCC TCC TGAGTGGCCA GCCTTTCCCC CTGTGAAAGC Val Gly Ile Ser Pro Ser 405	1248
AAAATAGCTT GGACCCCTTC AAGTTGAGAA CTGGTCAGGG CAAACCTGCC TCCCATTCTA	1308
CTCAAAGTCA TCCCTCTGCT CACAGAGATG GATGCATGTT CTGATTGCCT CTTTGGAGAA	1368
GCTCATCAGA AACTCAAAAG AAGGCCACTG TTTGTCTCAC CTACCCATGA CCTGAAGCCC	1428
CTCCCTGAGT GGTCCCCACC TTTCTGGACG GAACCACGTA CTTTTTACAT ACATTGATTC	1488
ATGTCTCACG TCTCCCTAAA AATGCGTAAG ACCAAGCTGT GCCCTGACCA CCCTGGGCCC	1548
CTGTCGTCAG GACCTCCTGA GGCTTTGGCA AATAAACCTC CTAAAATGAT AAAAAAAAAA	1608
AAAAAAAAAA AAAAAA	1624

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Asp	Phe	Gly	Leu	Ala	Leu	Leu	Leu	Ala	Gly	Leu	Leu	Gly	Leu	Leu
1				5					10					15	

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Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu Pro Pro Glu
 20 25 30
 Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg
 35 40 45
 Leu Ala Cys Ala Asp Arg Gly Ala Ser Val Gln Trp Arg Gly Leu Asp
 50 55 60
 Thr Ser Leu Gly Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr
 65 70 75 80
 Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val Cys Val Gly
 85 90 95
 Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Gln Leu Leu Val Tyr
 100 105 110
 Ala Phe Pro Asp Gln Leu Thr Val Ser Pro Ala Ala Leu Val Pro Gly
 115 120 125
 Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro Val Asp Pro
 130 135 140
 Asn Ala Leu Ser Phe Ser Leu Leu Val Gly Gly Gln Glu Leu Glu Gly
 145 150 155 160
 Ala Gln Ala Leu Gly Pro Glu Val Gln Glu Glu Glu Glu Pro Gln
 165 170 175
 Gly Asp Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp Arg Leu Pro
 180 185 190
 Pro Leu Gly Thr Pro Val Pro Pro Ala Leu Tyr Cys Gln Ala Thr Met
 195 200 205
 Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala Ile Pro Val Leu
 210 215 220
 His Ser Pro Thr Ser Pro Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro
 225 230 235 240
 Pro Asn Thr Thr Ser Pro Glu Ser Pro Asp Thr Thr Ser Pro Glu Ser
 245 250 255
 Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Gln Glu Pro
 260 265 270
 Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro
 275 280 285
 Pro Asp Lys Thr Ser Pro Glu Pro Ala Pro Gln Gln Gly Ser Thr His
 290 295 300
 Thr Pro Arg Ser Pro Gly Ser Thr Arg Thr Arg Arg Pro Glu Ile Ser
 305 310 315 320
 Gln Ala Gly Pro Thr Gln Gly Glu Val Ile Pro Thr Gly Ser Ser Lys
 325 330 335
 Pro Ala Gly Asp Gln Leu Pro Ala Ala Leu Trp Thr Ser Ser Ala Val
 340 345 350

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Leu Gly Leu Leu Leu Leu Ala Leu Pro Thr Tyr His Leu Trp Lys Arg
 355 360 365
 Cys Arg His Leu Ala Glu Asp Asp Thr His Pro Pro Ala Ser Leu Arg
 370 375 380
 Leu Leu Pro Gln Val Ser Ala Trp Ala Gly Leu Arg Gly Thr Gly Gln
 385 390 395 400
 Val Gly Ile Ser Pro Ser
 405

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1539 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GAT TTC GGA CTG GCC CTC CTG CTG GCG GGG CTT CTG GGG CTC CTC	48
Met Asp Phe Gly Leu Ala Leu Leu Leu Ala Gly Leu Leu Gly Leu Leu	
1 5 10 15	
CTC GGC CAG TCC CTC CAG GTG AAG CCC CTG CAG GTG GAG CCC CCG GAG	96
Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu Pro Pro Glu	
20 25 30	
CCG GTG GTG GCC GTG GCC TTG GGC GCC TCG CGC CAG CTC ACC TGC CGC	144
Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg	
35 40 45	
CTG GCC TGC GCG GAC CGC GGG GCC TCG GTG CAG TGG CGG GGC CTG GAC	192
Leu Ala Cys Ala Asp Arg Gly Ala Ser Val Gln Trp Arg Gly Leu Asp	
50 55 60	
ACC AGC CTG GGC GCG GTG CAG TCG GAC ACG GGC CGC AGC GTC CTC ACC	240
Thr Ser Leu Gly Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr	
65 70 75 80	
GTG CGC AAC GCC TCG CTG TCG GCG GCC GGG ACC CGC GTG TGC GTG GGC	288
Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val Cys Val Gly	
85 90 95	
TCC TGC GGG GGC CGC ACC TTC CAG CAC ACC GTG CAG CTC CTT GTG TAC	336
Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Gln Leu Leu Val Tyr	
100 105 110	

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GCC TTC CCG GAC CAG CTG ACC GTC TCC CCA GCA GCC CTG GTG CCT GGT Ala Phe Pro Asp Gln Leu Thr Val Ser Pro Ala Ala Leu Val Pro Gly 115 120 125	384
GAC CCG GAG GTG GCC TGT ACG GCC CAC AAA GTC ACG CCC GTG GAC CCC Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro Val Asp Pro 130 135 140	432
AAC GCG CTC TCC TTC TCC CTG CTC GTC GGG GGC CAG GAA CTG GAG GGG Asn Ala Leu Ser Phe Ser Leu Leu Val Gly Gly Gln Glu Leu Glu Gly 145 150 155 160	480
GCG CAA GCC CTG GGC CCG GAG GTG CAG GAG GAG GAG GAG CCC CAG Ala Gln Ala Leu Gly Pro Glu Val Gln Glu Glu Glu Glu Pro Gln 165 170 175	528
GGG GAC GAG GAC GTG CTG TTC AGG GTG ACA GAG CGC TGG CCG CTG CCG Gly Asp Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp Arg Leu Pro 180 185 190	576
CCC CTG GGG ACC CCT GTC CCG CCC GCC CTC TAC TGC CAG GCC ACG ATG Pro Leu Gly Thr Pro Val Pro Pro Ala Leu Tyr Cys Gln Ala Thr Met 195 200 205	624
AGG CTG CCT GGC TTG GAG CTC AGC CAC CGC CAG GCC ATC CCC GTC CTG Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala Ile Pro Val Leu 210 215 220	672
CAC AGC CCG ACC TCC CCG GAG CCT CCC GAC ACC ACC TCC CCG GAG TCT His Ser Pro Thr Ser Pro Glu Pro Pro Asp Thr Thr Ser Pro Glu Ser 225 230 235 240	720
CCC GAC ACC ACC TCC CCG GAG TCT CCC GAC ACC ACC TCC CAG GAG CCT Pro Asp Thr Thr Ser Pro Glu Ser Pro Asp Thr Thr Ser Gln Glu Pro 245 250 255	768
CCC GAC ACC ACC TCC CCG GAG CCT CCC GAC AAG ACC TCC CCG GAG CCC Pro Asp Thr Thr Ser Pro Glu Pro Pro Asp Lys Thr Ser Pro Glu Pro 260 265 270	816
GCC CCC CAG CAG GGC TCC ACA CAC ACC CCC AGG AGC CCA GGC TCC ACC Ala Pro Gln Gln Gly Ser Thr His Thr Pro Arg Ser Pro Gly Ser Thr 275 280 285	864
AGG ACT CGC CGC CCT GAG ATC TCC CAG GCT GGG CCC ACG CAG GGA GAA Arg Thr Arg Arg Pro Glu Ile Ser Gln Ala Gly Pro Thr Gln Gly Glu 290 295 300	912
GTG ATC CCA ACA GGC TCG TCC AAA CCT GCG GGT GAC CAG CTG CCC GCG Val Ile Pro Thr Gly Ser Ser Lys Pro Ala Gly Asp Gln Leu Pro Ala 305 310 315 320	960
GCT CTG TGG ACC AGC AGT GCG GTG CTG GGA CTG CTG CTC CTG GCC TTG Ala Leu Trp Thr Ser Ser Ala Val Leu Gly Leu Leu Leu Leu Ala Leu 325 330 335	1008
CCC ACC TAT CAC CTC TGG AAA CGC TGC CGG CAC CTG GCT GAG GAC GAC Pro Thr Tyr His Leu Trp Lys Arg Cys Arg His Leu Ala Glu Asp Asp 340 345 350	1056

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ACC CAC CCA CCA GCT TCT CTG AGG CTT CTG CCC CAG GTG TCG GCC TGG	1104
Thr His Pro Pro Ala Ser Leu Arg Leu Leu Pro Gln Val Ser Ala Trp	
355 360 365	
GCT GGG TTA AGG GGG ACC GGC CAG GTC GGG ATC AGC CCC TCC	1146
Ala Gly Leu Arg Gly Thr Gly Gln Val Gly Ile Ser Pro Ser	
370 375 380	
TGAGTGGCCA GCCTTTCCCC CTGTGAAAGC AAAATAGCTT GGACCCCTTC AAGTTGAGAA	1206
CTGGTCAGGG CAAACCTGCC TCCCATTCTA CTCAAAGTCA TCCCTCTGTT CACAGAGATG	1266
GATGCATGTT CTGATTGCCT CTTTGGAGAA GCTCATCAGA AACTCAAAAG AAGGCCACTG	1326
TTTGTCTCAC CTACCCATGA CCTGAAGCCC CTCCCTGAGT GGTCCCCACC TTTCTGGACG	1386
GAACCACGTA CTTTTTACAT ACATTGATTC ATGTCTCAGG TCTCCCTAAA AATGCGTAAG	1446
ACCAAGCTGT GCCCTGACCA CCCTGGGCCC CTGTCGTGAG GACCTCCTGA GGCTTTGGCA	1506
AATAAACCTC CTAAATGAA AAAAAAAAAA AAA	1539

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asp	Phe	Gly	Leu	Ala	Leu	Leu	Leu	Ala	Gly	Leu	Leu	Gly	Leu	Leu
1				5					10					15	
Leu	Gly	Gln	Ser	Leu	Gln	Val	Lys	Pro	Leu	Gln	Val	Glu	Pro	Pro	Glu
		20					25					30			
Pro	Val	Val	Ala	Val	Ala	Leu	Gly	Ala	Ser	Arg	Gln	Leu	Thr	Cys	Arg
		35				40						45			
Leu	Ala	Cys	Ala	Asp	Arg	Gly	Ala	Ser	Val	Gln	Trp	Arg	Gly	Leu	Asp
	50				55						60				
Thr	Ser	Leu	Gly	Ala	Val	Gln	Ser	Asp	Thr	Gly	Arg	Ser	Val	Leu	Thr
65				70					75					80	
Val	Arg	Asn	Ala	Ser	Leu	Ser	Ala	Ala	Gly	Thr	Arg	Val	Cys	Val	Gly
			85					90					95		
Ser	Cys	Gly	Gly	Arg	Thr	Phe	Gln	His	Thr	Val	Gln	Leu	Leu	Val	Tyr
		100					105					110			
Ala	Phe	Pro	Asp	Gln	Leu	Thr	Val	Ser	Pro	Ala	Ala	Leu	Val	Pro	Gly
		115				120						125			

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Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro Val Asp Pro
 130 135 140
 Asn Ala Leu Ser Phe Ser Leu Leu Val Gly Gly Gln Glu Leu Glu Gly
 145 150 155 160
 Ala Gln Ala Leu Gly Pro Glu Val Gln Glu Glu Glu Glu Pro Gln
 165 170 175
 Gly Asp Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp Arg Leu Pro
 180 185 190
 Pro Leu Gly Thr Pro Val Pro Pro Ala Leu Tyr Cys Gln Ala Thr Met
 195 200 205
 Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala Ile Pro Val Leu
 210 215 220
 His Ser Pro Thr Ser Pro Glu Pro Pro Asp Thr Thr Ser Pro Glu Ser
 225 230 235 240
 Pro Asp Thr Thr Ser Pro Glu Ser Pro Asp Thr Thr Ser Gln Glu Pro
 245 250 255
 Pro Asp Thr Thr Ser Pro Glu Pro Pro Asp Lys Thr Ser Pro Glu Pro
 260 265 270
 Ala Pro Gln Gln Gly Ser Thr His Thr Pro Arg Ser Pro Gly Ser Thr
 275 280 285
 Arg Thr Arg Arg Pro Glu Ile Ser Gln Ala Gly Pro Thr Gln Gly Glu
 290 295 300
 Val Ile Pro Thr Gly Ser Ser Lys Pro Ala Gly Asp Gln Leu Pro Ala
 305 310 315 320
 Ala Leu Trp Thr Ser Ser Ala Val Leu Gly Leu Leu Leu Leu Ala Leu
 325 330 335
 Pro Thr Tyr His Leu Trp Lys Arg Cys Arg His Leu Ala Glu Asp Asp
 340 345 350
 Thr His Pro Pro Ala Ser Leu Arg Leu Leu Pro Gln Val Ser Ala Trp
 355 360 365
 Ala Gly Leu Arg Gly Thr Gly Gln Val Gly Ile Ser Pro Ser
 370 375 380

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1721 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 4..1038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGC	ATG	GAT	CGG	GGC	CTG	GCC	CTC	CTG	CTG	GCG	GGG	CTT	CTG	GGG	CTC	48
Met	Asp	Arg	Gly	Leu	Ala	Leu	Leu	Leu	Ala	Gly	Leu	Leu	Gly	Leu		
1				5					10					15		
CTC	CAG	CCG	GGC	TGC	GGC	CAG	TCC	CTC	CAG	GTG	AAG	CCC	CTG	CAG	GTG	96
Leu	Gln	Pro	Gly	Cys	Gly	Gln	Ser	Leu	Gln	Val	Lys	Pro	Leu	Gln	Val	
			20					25						30		
GAG	CCC	CCG	GAG	CCG	GTG	GTG	GCC	GTG	GCC	CTG	GGC	GCC	TCT	CGC	CAG	144
Glu	Pro	Pro	Glu	Pro	Val	Val	Ala	Val	Ala	Leu	Gly	Ala	Ser	Arg	Gln	
			35					40					45			
CTC	ACC	TGC	CGC	CTG	GAC	TGC	GCG	GAC	CGC	GGG	GCC	ACG	GTG	CAG	TGG	192
Leu	Thr	Cys	Arg	Leu	Asp	Cys	Ala	Asp	Arg	Gly	Ala	Thr	Val	Gln	Trp	
		50					55					60				
CGG	GGC	CTG	GAC	ACC	AGC	CTG	GGC	GCG	GTG	CAG	TCG	GAC	GCG	GGC	CGC	240
Arg	Gly	Leu	Asp	Thr	Ser	Leu	Gly	Ala	Val	Gln	Ser	Asp	Ala	Gly	Arg	
	65					70				75						
AGC	GTC	CTC	ACC	GTG	CGC	AAC	GCC	TCG	CTG	TCG	GCG	GCC	GGG	ACC	CGT	288
Ser	Val	Leu	Thr	Val	Arg	Asn	Ala	Ser	Leu	Ser	Ala	Ala	Gly	Thr	Arg	
	80				85				90						95	
GTG	TGC	GTG	GGC	TCC	TGC	GGG	GGC	CGC	ACC	TTC	CAG	CAC	ACC	GTG	CGG	336
Val	Cys	Val	Gly	Ser	Cys	Gly	Gly	Arg	Thr	Phe	Gln	His	Thr	Val	Arg	
			100					105						110		
CTC	CTT	GTG	TAC	GCC	TTC	CCG	GAC	CAG	CTG	ACC	ATC	TCC	CCG	GCA	GCC	384
Leu	Leu	Val	Tyr	Ala	Phe	Pro	Asp	Gln	Leu	Thr	Ile	Ser	Pro	Ala	Ala	
			115					120					125			
CTG	GTG	CCT	GGT	GAC	CCG	GAG	GTG	GCC	TGT	ACG	GCC	CAC	AAA	GTC	ACG	432
Leu	Val	Pro	Gly	Asp	Pro	Glu	Val	Ala	Cys	Thr	Ala	His	Lys	Val	Thr	
		130				135					140					
CCT	GTG	GAC	CCC	AAT	GCG	CTC	TCC	TTC	TCC	CTG	CTC	CTG	GGG	GAC	CAG	480
Pro	Val	Asp	Pro	Asn	Ala	Leu	Ser	Phe	Ser	Leu	Leu	Leu	Gly	Asp	Gln	
		145				150					155					
GAA	CTG	GAG	GGG	GCC	CAG	GCT	CTG	GGC	CCG	GAG	GTG	GAG	GAG	GAG	GAG	528
Glu	Leu	Glu	Gly	Ala	Gln	Ala	Leu	Gly	Pro	Glu	Val	Glu	Glu	Glu	Glu	
	160				165				170						175	
GAG	GAG	CCC	CAG	GAG	GAG	GAG	GAC	GTG	CTG	TTC	AGG	GTG	ACA	GAG	CGC	576
Glu	Glu	Pro	Gln	Glu	Glu	Glu	Asp	Val	Leu	Phe	Arg	Val	Thr	Glu	Arg	
			180					185						190		
TGG	CGG	CTG	CCG	ACC	CTG	GCA	ACC	CCT	GTC	CTG	CCC	GCG	CTC	TAC	TGC	624
Trp	Arg	Leu	Pro	Thr	Leu	Ala	Thr	Pro	Val	Leu	Pro	Ala	Leu	Tyr	Cys	
			195					200					205			

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CAG GCC ACG ATG AGG CTG CCT GGC TTG GAG CTC AGC CAC CGC CAG GCC Gln Ala Thr Met Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala 210 215 220	672
ATC CCG GTC CTG CAC GGC CCG ACC TCC CGG GAG CCC CCC GAC ACG ACC Ile Pro Val Leu His Gly Pro Thr Ser Arg Glu Pro Pro Asp Thr Thr 225 230 235	720
TCC CCG GAA CCC CGG GCC GCG ACC TCC CCG GAG ACC ACC CCC CAG CAG Ser Pro Glu Pro Arg Ala Ala Thr Ser Pro Glu Thr Thr Pro Gln Gln 240 245 250 255	768
GGC TCC ACA CAC AGC CCC AGG AGC CCG GGC TCT ACC AGG ACT TGC CGC Gly Ser Thr His Ser Pro Arg Ser Pro Gly Ser Thr Arg Thr Cys Arg 260 265 270	816
CCT GAG ATC TCC CAG GCT GGG CCC ACG CAG GGA GAA GTG ATC CCA ACA Pro Glu Ile Ser Gln Ala Gly Pro Thr Gln Gly Glu Val Ile Pro Thr 275 280 285	864
GGC TCG TCC AAA CCT ACG GGT GAC CAG CTG CCC GCG GCT CTG TGG ACC Gly Ser Ser Lys Pro Thr Gly Asp Gln Leu Pro Ala Ala Leu Trp Thr 290 295 300	912
AGC AGT GCG GTG CTG GGA CTG CTG CTC CTG GCT TTG CCC ACC TAC CAC Ser Ser Ala Val Leu Gly Leu Leu Leu Leu Ala Leu Pro Thr Tyr His 305 310 315	960
CTC TGG AAA CGT TGC CGG CAC CTG GCT GAG GAC GGC GCC CAC CCA CCA Leu Trp Lys Arg Cys Arg His Leu Ala Glu Asp Gly Ala His Pro Pro 320 325 330 335	1008
GCT TCT CTG AGT AGC CAG CCC TTC CCC CTG TGAAGGGAAA ATAGGTTGGA Ala Ser Leu Ser Ser Gln Pro Phe Pro Leu 340 345	1058
CCCCTTCAAG CTGAGAACTG GTCGGGGCAA ACCTGCCTCC CATTCTATTC AAAGTCATCG	1118
CTCTGGTCAC AGAGAGGGGAC GCACATTCTG ATTGCCTCCT TTGGAAAGGC TCATCAGAAA	1178
CTCAAAAGAA GGTGATCGTT TGTCCCGCCT ACCCGTGACC TGGAAGCCCC CGCCCCGCTC	1238
GAGTGACCCC TGACTTTCTG GACGGAACCA ACGTACTTCT TACATATATT GATTCATGTG	1298
TCATATCTCC CTAAAATGCG TAAAACCAGC TGTGCCCCGA CCACCTTGGG CCCCTGCCAT	1358
CAGGACCTCC TGAGGCTTTG GCAAATAAAC CTCCTAAAAG GATAGAACT GAAACTTGTG	1418
GCCGGGCGCG GTGGCTCAAG CCTGTAATCC CAGCACTTTG GGAGGCCGAG GTGGGTGGAT	1478
CACGAGGTCA GGAGATCGAG ACCATCCTGG CTAACCCGTG AAACCCCGTC TCTACTAAAA	1538
AAATACAAAA ATTAGCCGGG AGCGGTGGCG GCGCCTGTA GTCCAGCTA CTCGGGAGGC	1598
TGAGGCAGGA GAATGGCGTG AACCCGGGAG GCGGAGCTTG CAGTGAGCTG AGATCCGGCC	1658
ACTGCACTCC AGCCTGGGGG ACAGAGCGAG ACTCCGTCTC AAAAAAAAAA AAAAAAAAAA	1718
AAA	1721

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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Met Asp Arg Gly Leu Ala Leu Leu Leu Ala Gly Leu Leu Gly Leu Leu
 1           5           10           15
Gln Pro Gly Cys Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu
 20           25           30
Pro Pro Glu Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu
 35           40           45
Thr Cys Arg Leu Asp Cys Ala Asp Arg Gly Ala Thr Val Gln Trp Arg
 50           55           60
Gly Leu Asp Thr Ser Leu Gly Ala Val Gln Ser Asp Ala Gly Arg Ser
 65           70           75           80
Val Leu Thr Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val
 85           90           95
Cys Val Gly Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Arg Leu
 100          105          110
Leu Val Tyr Ala Phe Pro Asp Gln Leu Thr Ile Ser Pro Ala Ala Leu
 115          120          125
Val Pro Gly Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro
 130          135          140
Val Asp Pro Asn Ala Leu Ser Phe Ser Leu Leu Leu Gly Asp Gln Glu
 145          150          155          160
Leu Glu Gly Ala Gln Ala Leu Gly Pro Glu Val Glu Glu Glu Glu Glu
 165          170          175
Glu Pro Gln Glu Glu Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp
 180          185          190
Arg Leu Pro Thr Leu Ala Thr Pro Val Leu Pro Ala Leu Tyr Cys Gln
 195          200          205
Ala Thr Met Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala Ile
 210          215          220
Pro Val Leu His Gly Pro Thr Ser Arg Glu Pro Pro Asp Thr Thr Ser
 225          230          235          240
Pro Glu Pro Arg Ala Ala Thr Ser Pro Glu Thr Thr Pro Gln Gln Gly
 245          250          255

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Ser Thr His Ser Pro Arg Ser Pro Gly Ser Thr Arg Thr Cys Arg Pro
 260 265 270

Glu Ile Ser Gln Ala Gly Pro Thr Gln Gly Glu Val Ile Pro Thr Gly
 275 280 285

Ser Ser Lys Pro Thr Gly Asp Gln Leu Pro Ala Ala Leu Trp Thr Ser
 290 295 300

Ser Ala Val Leu Gly Leu Leu Leu Leu Ala Leu Pro Thr Tyr His Leu
 305 310 315 320

Trp Lys Arg Cys Arg His Leu Ala Glu Asp Gly Ala His Pro Pro Ala
 325 330 335

Ser Leu Ser Ser Gln Pro Phe Pro Leu
 340 345

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTCTACTGCC AGGCCACG

18

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGCCTGGGAG ATCTCAGGG

19

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCCACGATGA GGCTGCCTGG

20

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(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTGGAGCCTG GGCTCCTGGG

20

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGAAGCTTCC ACCATGGATT TCGGACTGGC CC

32

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCGACTAGTG TCGGGCTGTG CAGGAC

26

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGACTAGTGG TTTGGACGAG CCTGTTG

27